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PATENT APPLICATION: US/09/769,736

DATE: 02/24/2003

TIME: 08:08:08

Input Set : A:\P21089WO.txt

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3 <110> APPLICANT: Microbial Technics Limited
 4 Le Page, Richard WF
 5 Wells, Jeremy M
 6 Hanniffy, Sean B
 8 <120> TITLE OF INVENTION: Proteins
 10 <130> FILE REFERENCE: PWC/P21089wo
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/769,736
 C--> 13 <141> CURRENT FILING DATE: 2003-02-14
 15 <150> PRIOR APPLICATION NUMBER: GB 9816335.5
 16 <151> PRIOR FILING DATE: 1998-07-27
 18 <150> PRIOR APPLICATION NUMBER: US 60/125163
 19 <151> PRIOR FILING DATE: 1999-03-19
 21 <160> NUMBER OF SEQ ID NOS: 212
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1248
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Streptococcus agalactiae
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 33 aaactttggg tcccaacaga ttcaaaagcg tcttataaag caattggtta aaaattcgag 180
 34 aaggaaaaaca aaggcggttac tgtaaaaatg attgagtcta atgactccaa agctcaagaa 240
 35 aacgtaaaaa aagaccaag caaggcagcc gatgtattct cacttccaca tgaccaactt 300
 36 ggtcaattag tagaatctgg tgttatccaa gaaattccag agcaatactc aaaagaaatt 360
 37 gctaaaaacg aactaaaca atcaacttact ggtgcacaat ataaaggga aacttatgca 420
 38 ttcccatttg gtattgaatc tcaagttctt tattataata aaacaaagt aactgctgac 480
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 42 tggattgcag atcaaaagaa aaatgatggt tttgtcaact tgacagctga aaatacaatg 720
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 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 415
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59 <400> SEQUENCE: 2

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64           20           25           30
66 Asp Ala Ala Ser Lys Lys Thr Ile Lys Leu Trp Val Pro Thr Asp Ser
67           35           40           45
69 Lys Ala Ala Ser Tyr Lys Ala Ile Val Lys Lys Phe Glu Lys Glu Asn Lys
70           50           55           60
72 Gly Val Thr Val Lys Met Ile Glu Ser Asn Asp Ser Lys Ala Gln Glu
73           65           70           75           80
75 Asn Val Lys Lys Asp Pro Ser Lys Ala Ala Asp Val Phe Ser Leu Pro
76           85           90           95
78 His Asp Gln Leu Gly Gln Leu Val Glu Ser Gly Val Ile Gln Glu Ile
79           100          105          110
81 Pro Glu Gln Tyr Ser Lys Glu Ile Ala Lys Asn Asp Thr Lys Gln Ser
82           115          120          125
84 Leu Thr Gly Ala Gln Tyr Lys Gly Lys Thr Tyr Ala Phe Pro Phe Gly
85           130          135          140
87 Ile Glu Ser Gln Val Leu Tyr Tyr Asn Lys Thr Lys Leu Thr Ala Asp
88          145          150          155          160
90 Asp Val Lys Ser Tyr Glu Thr Ile Thr Ser Lys Gly Lys Phe Gly Gln
91           165          170          175
93 Gln Leu Lys Ala Ala Asn Ser Tyr Val Thr Gly Pro Leu Phe Leu Ser
94           180          185          190
96 Val Gly Asp Thr Leu Phe Gly Lys Ser Gly Glu Asp Ala Lys Gly Thr
97           195          200          205
99 Asn Trp Gly Asn Glu Ala Gly Val Ser Val Leu Lys Trp Ile Ala Asp
100          210          215          220
102 Gln Lys Lys Asn Asp Gly Phe Val Asn Leu Thr Ala Glu Asn Thr Met
103          225          230          235          240
105 Ser Lys Phe Gly Asp Gly Ser Val His Ala Phe Glu Ser Gly Pro Trp
106           245          250          255
108 Asp Tyr Asp Ala Ala Lys Lys Ala Val Gly Glu Asp Lys Ile Gly Val
109           260          265          270
111 Ala Val Tyr Pro Thr Met Lys Ile Gly Asp Lys Glu Val Gln Gln Lys
112           275          280          285
114 Ala Phe Leu Gly Val Lys Leu Tyr Ala Val Asn Gln Ala Pro Ala Gly
115           290          295          300
117 Ser Asn Thr Lys Arg Ile Ser Ala Ser Tyr Lys Leu Ala Ala Tyr Leu
118          305          310          315          320
120 Thr Asn Ala Glu Ser Gln Lys Ile Gln Phe Glu Lys Arg His Ile Val
121           325          330          335
123 Pro Ala Asn Ser Ser Ile Gln Ser Ser Asp Ser Val Gln Lys Asp Glu
124           340          345          350
126 Leu Ala Lys Ala Val Ile Glu Met Gly Ser Ser Asp Lys Tyr Thr Thr
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130      370      375      380
132 Ala Ile Leu Ser Asp Thr Tyr Ser Gly Lys Ile Lys Ser Ser Asp Tyr
133 385      390      395      400
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142 <212> TYPE: DNA
143 <213> ORGANISM: Streptococcus agalactiae
145 <400> SEQUENCE: 3
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147 tcaccttttag tgaccttagc agaaactatt aatccagaaa caagcctgac aatggcaaca 120
148 gcatcaacag aaagtctctt tgaagcagag aaacaggaaa aaacacaacc tacagattca 180
149 gaaactgctt caccttcagc cgaaggaagt atctcaacag aaaaaacaga gattggtacg 240
150 acagagacat catcaagcaa tgaatcatca tcaagttcat cacatcaatc ttcttccaac 300
151 gaagatgcta aaacatctga ttctgcttca acagcatcta ctcttagcac taatactaca 360
152 aacagtagtc aagcagacag taagccaggt caatcaacaa agactgaatt aaaacctgag 420
153 cctaccttac cattagtaga gcctaaaata actcccgctc cgtctcagat agaaagtgtt 480
154 cagacaaatc agaatgcttc tgttctgctt ttatcctttg atgataactt attatcaaca 540
155 ccgatttcac cagtgcacgc aacgccattc tacgtagaac actggtctgg tcaggatgcc 600
156 tactctcact atttattgtc acatcgttac ggtatcaaaag ctgaacaatt agatgggtac 660
157 ttaaaatctt tagggattca atatgattct aatcgtagta atgggtgctaa gttattacaa 720
158 tgggaaaaag atagtgggtt agatgtccgt gctattgtag ctattgctgt ccttgaaagt 780
159 tcattgggaa ctcaaggagt ggctaaaatg ccagggtgcta atatggttggt ttatgggtgcc 840
160 tttgatcatg actctagcca tgctagtgtt tataatgatg aagaagcaat tatgttggtg 900
161 acaaaaaata caattattaa aaacaacaac tctagctttg aaatccaaga tttgaaagca 960
162 cagaaattat cttctggaca acttaataca gttactgagg gtggtgttta ttatacagat 1020
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187      35      40      45
189 Ala Glu Lys Gln Glu Lys Thr Gln Pro Thr Asp Ser Glu Thr Ala Ser
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199 100 105 110
201 Ser Thr Pro Ser Thr Asn Thr Thr Asn Ser Ser Gln Ala Asp Ser Lys
202 115 120 125
204 Pro Gly Gln Ser Thr Lys Thr Glu Leu Lys Pro Glu Pro Thr Leu Pro
205 130 135 140
207 Leu Val Glu Pro Lys Ile Thr Pro Ala Pro Ser Gln Ile Glu Ser Val
208 145 150 155 160
210 Gln Thr Asn Gln Asn Ala Ser Val Pro Ala Leu Ser Phe Asp Asp Asn
211 165 170 175
213 Leu Leu Ser Thr Pro Ile Ser Pro Val Thr Ala Thr Pro Phe Tyr Val
214 180 185 190
216 Glu His Trp Ser Gly Gln Asp Ala Tyr Ser His Tyr Leu Leu Ser His
217 195 200 205
219 Arg Tyr Gly Ile Lys Ala Glu Gln Leu Asp Gly Tyr Leu Lys Ser Leu
220 210 215 220
222 Gly Ile Gln Tyr Asp Ser Asn Arg Ile Asn Gly Ala Lys Leu Leu Gln
223 225 230 235 240
225 Trp Glu Lys Asp Ser Gly Leu Asp Val Arg Ala Ile Val Ala Ile Ala
226 245 250 255
228 Val Leu Glu Ser Ser Leu Gly Thr Gln Gly Val Ala Lys Met Pro Gly
229 260 265 270
231 Ala Asn Met Phe Gly Tyr Gly Ala Phe Asp His Asp Ser Ser His Ala
232 275 280 285
234 Ser Ala Tyr Asn Asp Glu Glu Ala Ile Met Leu Leu Thr Lys Asn Thr
235 290 295 300
237 Ile Ile Lys Asn Asn Asn Ser Ser Phe Glu Ile Gln Asp Leu Lys Ala
238 305 310 315 320
240 Gln Lys Leu Ser Ser Gly Gln Leu Asn Thr Val Thr Glu Gly Gly Val
241 325 330 335
243 Tyr Tyr Thr Asp Asn Ser Gly Thr Gly Lys Arg Arg Ala Gln Ile Met
244 340 345 350
246 Glu Asp Leu Asp Arg Trp Ile Asp Gln His Gly Gly Thr Pro Glu Ile
247 355 360 365
249 Pro Ala Ala Leu Lys Ala Leu Ser Thr Ala Ser Leu Ala Asp Leu Pro
250 370 375 380
252 Ser Gly Phe Ser Leu Ser Thr Ala Val Asn Thr Ala Ser Tyr Ile Ala
253 385 390 395 400
255 Ser Thr Tyr Pro Trp Gly Glu Cys Thr Trp Tyr Val Phe Asn Arg Ala
256 405 410 415
258 Lys Glu Leu Gly Tyr Thr Phe Asp Pro Phe Met Gly Asn Gly Gly Asp
259 420 425 430
261 Trp Gln His Lys Ala Gly Phe Glu Thr Thr His Ser Pro Lys Val Gly
262 435 440 445
264 Tyr Ala Val Ser Phe Ser Pro Gly Gln Ala Gly Ala Asp Gly Thr Tyr

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270 Ile Ser Glu Ser Asn Ala Met Gly Arg Gly Ile Val Ser Tyr Arg Thr
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282 <211> LENGTH: 1293
283 <212> TYPE: DNA
284 <213> ORGANISM: Streptococcus agalactiae
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289 gatttgggta ttataaataa taaagtgcaa gaaagtgtct ctggcgtaa agtgactaaa 180
290 tcattgtgtt atcaagaaca agaaattgct tcttttcaag agattaatca gatgactttc 240
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323 Glu Glu Val Val Gly Thr Ala Leu Asp Leu Gly Ile Ile Asn Asn Lys
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326 Val Gln Glu Ser Val Ser Gly Val Lys Val Thr Lys Ser Leu Cys Tyr
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VERIFICATION SUMMARY

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DATE: 02/24/2003

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